

WHAT IS CLAIMED:

1. An isolated nucleic acid molecule consisting essentially of a nucleic acid sequence of SEQ ID NO:2471, or a complement thereof.
2. An isolated nucleic acid molecule consisting essentially of a nucleic acid sequence of SEQ ID NO:2473, or a complement thereof.
3. An isolated nucleic acid molecule which hybridizes under stringent conditions to a nucleic acid molecule having the nucleotide sequence of claim 1 or 2, or a complement thereof.
4. The nucleic acid molecule of claim 1 or 2 wherein the molecule is RNA.
5. The nucleic acid molecule of claim 1 or 2 wherein the molecule is DNA.
6. An isolated nucleic acid molecule which hybridizes under stringent conditions to the nucleic acid molecule of claim 1 or 2, or a complement thereof, wherein the nucleic acid molecule encodes an amino acid sequence which has a biological activity exhibited by a polypeptide encoded by the nucleotide sequence of SEQ ID NO:2471 or 2473.
7. An isolated polypeptide encoded by the nucleic acid molecule of claim 1 or 2.
8. An antibody or an antigen-binding fragment thereof which immunospecifically binds to the N-gene protein of a hSARS virus.
9. An antibody or an antigen-binding fragment thereof which immunospecifically binds to the S-gene protein of a hSARS virus.
10. The antibody of claim 8, 9, or an antigen-binding fragment thereof which neutralizes the hSARS virus.
11. An antibody which immunospecifically binds to the polypeptide of claim 7, or an antigen-binding fragment of said antibody.
12. A method for detecting the presence of a N-gene of the hSARS virus in a biological sample, said method comprising:

- (a) contacting the sample with a compound that selectively binds to said N-gene; and
- (b) detecting whether the compound binds to said N-gene in the sample.

13. The method of claim 12, wherein the compound that binds to said N-gene is a nucleic acid molecule comprising a nucleotide sequence having at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150 or 1,200 contiguous nucleotides of the nucleotide sequence of SEQ ID NO:2471, or a complement thereof.

14. The method of claim 12, wherein the compound that binds to said N-gene is a nucleic acid molecule comprising a nucleotide sequence of SEQ ID NO:2475, 2476, 2480 and/or 2481.

15. A method for detecting the presence of a S-gene of the hSARS virus in a biological sample, said method comprising:

- (a) contacting the sample with a compound that selectively binds to said S-gene; and
- (b) detecting whether the compound binds to said S-gene in the sample.

16. The method of claim 15, wherein the compound that binds to said S-gene is a nucleic acid molecule comprising a nucleotide sequence having at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, 2,000, or 3,000 contiguous nucleotides of the nucleotide sequence of SEQ ID NO:2473, or a complement thereof.

17. The method of claim 15, wherein the compound that binds to said S-gene is a nucleic acid molecule comprising a nucleotide sequence of SEQ ID NO:2477 and/or 2478.

18. A method for detecting the presence of the polypeptide of claim 7 in a sample, said method comprising:

- (a) contacting the sample with a compound that selectively binds to said polypeptide; and

- (b) detecting whether the compound binds to said polypeptide in the sample.
- 19. The method of claim 18, wherein the compound that binds to the polypeptide is an antibody.
- 20. A method for identifying a subject infected with the hSARS virus, said method comprising:
 - (a) obtaining total RNA from a biological sample obtained from the subject
 - (b) reverse transcribing the total RNA to obtain cDNA; and
 - (c) subjecting the cDNA to real-time PCR assay using a set of primers derived from a nucleotide sequence of the N-gene of the hSARS.
- 21. The method of claim 20, wherein the set of primers have nucleotide sequences of SEQ ID NOS:2475 and 2476, respectively.
- 22. The method of claim 20, wherein the set of primers have nucleotide sequences of SEQ ID NOS:2480 and 2481, respectively.
- 23. A method for identifying a subject infected with the hSARS virus, said method comprising:
 - (a) obtaining total RNA from a biological sample obtained from the subject
 - (b) reverse transcribing the total RNA to obtain cDNA; and
 - (c) subjecting the cDNA to real-time PCR assay using a set of primers derived from a nucleotide sequence of the S-gene of the hSARS.
- 24. The method of claim 23, wherein the set of primers have nucleotide sequences of SEQ ID NOS:2477 and 2478, respectively.
- 25. A kit comprising in one or more containers one or more isolated nucleic acid molecules comprising a nucleotide sequence of SEQ ID NO:2475 and/or SEQ ID NO:2476.
- 26. A kit comprising in one or more containers one or more isolated nucleic acid molecules comprising a nucleotide sequence of SEQ ID NO:2480 and/or SEQ ID NO:2481.

27. A kit comprising in one or more containers one or more isolated nucleic acid molecules comprising a nucleotide sequence of SEQ ID NO:2477 and/or SEQ ID NO:2478.
28. A kit comprising in one or more containers one or more antibodies of claim 8 or 9.
29. A kit comprising in one or more containers one or more antibodies of claim 11.